

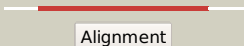

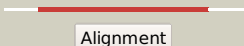







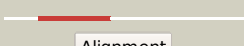











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3401 (-)_3818222_3820582
Date	Fri Aug 9 18:20:07 BST 2019
Unique Job ID	3f0f922c9c9dfd63

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ktrE_	 Alignment		100.0	25	PDB header: transferase Chain: E: PDB Molecule: glycoside hydrolase family 65 central catalytic; PDBTitle: crystal structure of 2-o-alpha-glycosylglycerol phosphorylase in2 complex with isofagomine and glycerol
2	c1h54B_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: maltose phosphorylase; PDBTitle: maltose phosphorylase from lactobacillus brevis
3	c2rdyB_	 Alignment		100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: bh0842 protein; PDBTitle: crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
4	c4ufcA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: gh95; PDBTitle: crystal structure of the gh95 enzyme bacova_03438
5	c2eacB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-fucosidase; PDBTitle: crystal structure of 1,2-a-l-fucosidase from2 bifidobacterium bifidum in complex with3 deoxyfuconojirimycin
6	d1h54a1	 Alignment		100.0	32	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
7	d1h54a2	 Alignment		100.0	20	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Glycosyltransferase family 36 N-terminal domain
8	c4zlgA_	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: putative b-glycan phosphorylase; PDBTitle: cellobionic acid phosphorylase - gluconic acid complex
9	c2cqtA_	 Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: cellobiose phosphorylase; PDBTitle: crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
10	c1v7wA_	 Alignment		100.0	11	PDB header: transferase Chain: A: PDB Molecule: chitobiose phosphorylase; PDBTitle: crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
11	d1v7wa1	 Alignment		100.0	13	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain

12	c5h42A_	Alignment		99.9	13	PDB header: transferase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 1,2-beta-oligoglucan phosphorylase from 2 lachnoclostridium phytofermentans in complex with alpha-d-glucose-1-3 phosphate
13	c6ggyA_	Alignment		99.9	15	PDB header: hydrolase Chain: A; PDB Molecule: laminaribiose phosphorylase; PDBTitle: paenibacillus sp. ym1 laminaribiose phosphorylase with sulphate bound
14	c5nz7A_	Alignment		99.9	12	PDB header: hydrolase Chain: A; PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase ligand free form
15	c5nz8A_	Alignment		99.8	15	PDB header: hydrolase Chain: A; PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
16	c6i60B_	Alignment		99.7	9	PDB header: hydrolase Chain: B; PDB Molecule: alpha-rhamnosidase; PDBTitle: structure of alpha-l-rhamnosidase from dictyoglumus thermophilum
17	c6gszA_	Alignment		99.7	13	PDB header: hydrolase Chain: A; PDB Molecule: alpha-l-rhamnosidase; PDBTitle: crystal structure of native alfa-l-rhamnosidase from aspergillus2 terreus
18	c2okxB_	Alignment		99.6	16	PDB header: hydrolase Chain: B; PDB Molecule: rhamnosidase b; PDBTitle: crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
19	c3cihA_	Alignment		99.5	13	PDB header: hydrolase Chain: A; PDB Molecule: putative alpha-rhamnosidase; PDBTitle: crystal structure of a putative alpha-rhamnosidase from 2 bacteroides thetaiotaomicron
20	c1ug9A_	Alignment		99.5	16	PDB header: hydrolase Chain: A; PDB Molecule: glucodextranase; PDBTitle: crystal structure of glucodextranase from arthrobacter globiformis i42
21	c1lf6A_	Alignment	not modelled	99.4	11	PDB header: hydrolase Chain: A; PDB Molecule: glucoamylase; PDBTitle: crystal structure of bacterial glucoamylase
22	c3w5mA_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A; PDB Molecule: putative rhamnosidase; PDBTitle: crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
23	c3c67B_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: B; PDB Molecule: uncharacterized protein ygjk; PDBTitle: escherichia coli k12 ygjk in a complexed with glucose
24	c5mqrA_	Alignment	not modelled	98.7	12	PDB header: hydrolase Chain: A; PDB Molecule: beta-l-arabinobiosidase; PDBTitle: sialidase bt_1020
25	c4xhcB_	Alignment	not modelled	98.7	16	PDB header: hydrolase Chain: B; PDB Molecule: alpha-l-rhamnosidase; PDBTitle: rhamnosidase from klebsiella oxytoxa with rhamnose bound
26	c5fjsB_	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: B; PDB Molecule: glucosylceramidase; PDBTitle: bacterial beta-glucosidase reveals the structural and functional2 basis of genetic defects in human glucocerebrosidase 2 (gba2)3 disorders
27	c2ww1B_	Alignment	not modelled	98.5	13	PDB header: hydrolase Chain: B; PDB Molecule: putative alpha-1,2-mannosidase; PDBTitle: structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
28	c5z3dA_	Alignment	not modelled	98.5	16	PDB header: hydrolase Chain: A; PDB Molecule: glycoside hydrolase 15-related protein; PDBTitle: glycosidase f290y
						PDB header: hydrolase

29	c2wvyA	Alignment	not modelled	98.0	15	Chain: A: PDB Molecule: alpha-1,2-mannosidase; PDBTitle: structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
30	c2jg0A	Alignment	not modelled	98.0	16	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic trehalase; PDBTitle: family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
31	d2jg0a1	Alignment	not modelled	98.0	16	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Trehalase-like
32	d1ulva1	Alignment	not modelled	97.8	15	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Bacterial glucoamylase C-terminal domain-like
33	c2z07A	Alignment	not modelled	97.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ttha0978; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
34	c6f92B	Alignment	not modelled	97.8	11	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-1,2-mannosidase; PDBTitle: structure of the family gh92 alpha-mannosidase bt3965 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)
35	d1lf6a1	Alignment	not modelled	97.7	13	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Bacterial glucoamylase C-terminal domain-like
36	c2zrzA	Alignment	not modelled	97.7	15	PDB header: hydrolase Chain: A: PDB Molecule: unsaturated glucuronyl hydrolase; PDBTitle: crystal structure of unsaturated glucuronyl hydrolase from2 streptococcus agalactiae
37	c5z73A	Alignment	not modelled	97.5	14	PDB header: hydrolase Chain: A: PDB Molecule: alr0819 protein; PDBTitle: crystal structure of alkaline/neutral invertase invb from anabaena sp.2 pcc 7120
38	d2d5ja1	Alignment	not modelled	97.4	16	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyl Hydrolase Family 88
39	c2vn4A	Alignment	not modelled	97.4	13	PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: glycoside hydrolase family 15 glucoamylase from hypocrea jecorina
40	c5swiD	Alignment	not modelled	97.2	11	PDB header: hydrolase Chain: D: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of spgh92 in complex with mannose
41	c6f90A	Alignment	not modelled	96.7	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha-1,2-mannosidase, putative; PDBTitle: structure of the family gh92 alpha-mannosidase bt3130 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)
42	c5gorE	Alignment	not modelled	96.7	14	PDB header: hydrolase Chain: E: PDB Molecule: alkaline invertase; PDBTitle: crystal structure of alkaline invertase inva from anabaena sp. pcc2 7120
43	c5n6nC	Alignment	not modelled	96.4	14	PDB header: signaling protein Chain: C: PDB Molecule: neutral trehalase; PDBTitle: crystal structure of the 14-3-3:neutral trehalase nth1 complex
44	c5mhfA	Alignment	not modelled	94.2	18	PDB header: hydrolase Chain: A: PDB Molecule: mannosyl-oligosaccharide glucosidase; PDBTitle: murine endoplasmic reticulum alpha-glucosidase i with n-9'-2 methoxyonyl-1-deoxynojirimycin
45	d1ulva4	Alignment	not modelled	94.1	15	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like
46	d1gaia	Alignment	not modelled	94.1	12	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glucoamylase
47	c6fhvA	Alignment	not modelled	93.9	13	PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: crystal structure of penicillium oxalicum glucoamylase
48	c6fhwB	Alignment	not modelled	93.7	11	PDB header: hydrolase Chain: B: PDB Molecule: glucoamylase p; PDBTitle: structure of hormoconis resinae glucoamylase
49	c5m4aA	Alignment	not modelled	93.6	11	PDB header: hydrolase Chain: A: PDB Molecule: neutral trehalase; PDBTitle: neutral trehalase nth1 from saccharomyces cerevisiae in complex with2 trehalose
50	c5d0fB	Alignment	not modelled	93.3	13	PDB header: sugar binding protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the candida glabrata glycogen debranching enzyme2 (e564q) in complex with maltopentaose
51	d1lf6a2	Alignment	not modelled	92.6	9	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like
52	c4qk0C	Alignment	not modelled	91.9	16	PDB header: hydrolase Chain: C: PDB Molecule: gh127 beta-l-arabinofuranoside; PDBTitle: crystal structure of ara127n-se, a gh127 beta-l-arabinofuranosidase2 from geobacillus stearothermophilus t6
53	c3wkxA	Alignment	not modelled	91.2	17	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end beta-l-arabinofuranosidase; PDBTitle: crystal structure of gh127 beta-l-arabinofuranosidase hypba1 from2 bifidobacterium longum arabinose complex form
54	d2fbaa1	Alignment	not modelled	91.1	18	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glucoamylase

55	c5uz9A_	Alignment	not modelled	80.7	20	PDB header: immune system/rna Chain: A: PDB Molecule: crispr-associated protein csy1; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crna-guided crispr surveillance complex
56	c2xsgB_	Alignment	not modelled	78.5	14	PDB header: hydrolase Chain: B: PDB Molecule: ccman5; PDBTitle: structure of the gh92 family glycosyl hydrolase ccman5
57	c3wiwA_	Alignment	not modelled	76.2	13	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 88; PDBTitle: crystal structure of unsaturated glucuronyl hydrolase specific for 2 heparin
58	c6ex6A_	Alignment	not modelled	71.6	15	PDB header: hydrolase Chain: A: PDB Molecule: six-hairpin glycosidase; PDBTitle: the gh127, beta-arabinofuranosidase, bt3674
59	c4mu9B_	Alignment	not modelled	67.8	19	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase family 73; PDBTitle: crystal structure of a putative glycosylhydrolase (bt_3782) from 2 bacteroides thetaiotaomicron vpi-5482 at 1.89 a resolution
60	c3vw5B_	Alignment	not modelled	58.2	13	PDB header: isomerase Chain: B: PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of sugar epimerase from ruminal bacterium
61	d1g9ga_	Alignment	not modelled	47.3	14	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
62	c2p0vA_	Alignment	not modelled	47.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bt3781; PDBTitle: crystal structure of bt3781 protein from bacteroides thetaiotaomicron,2 northeast structural genomics target btr58
63	d2p0va1	Alignment	not modelled	47.1	13	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
64	c4v1sA_	Alignment	not modelled	40.0	9	PDB header: hydrolase Chain: A: PDB Molecule: alpha-1,6-mannanase; PDBTitle: structure of the gh76 alpha-mannanase bt2949 from 2 bacteroides thetaiotaomicron
65	c5ohcB_	Alignment	not modelled	38.0	18	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: crystal structure of mycolicibacterium hassiacum glucosylglycerate2 hydrolase (mhggh) in complex with glycerol
66	c3qspB_	Alignment	not modelled	35.1	20	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
67	c4el8A_	Alignment	not modelled	33.1	18	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.bescii cela gh48 module
68	d1wgha_	Alignment	not modelled	29.6	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
69	c5zigD_	Alignment	not modelled	27.8	14	PDB header: isomerase Chain: D: PDB Molecule: cellobiose 2-epimerase; PDBTitle: the structure of cellobiose 2-epimerase from spirochaeta thermophila2 dsm 6192
70	c5hopA_	Alignment	not modelled	26.2	19	PDB header: hydrolase Chain: A: PDB Molecule: lmo0182 protein; PDBTitle: 1.65 angstrom resolution crystal structure of lmo0182 (residues 1-245)2 from listeria monocytogenes egd-e
71	c4jijA_	Alignment	not modelled	23.4	18	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of t. fusca gh48 d224n mutant
72	c4j5tA_	Alignment	not modelled	23.3	13	PDB header: hydrolase Chain: A: PDB Molecule: mannosyl-oligosaccharide glucosidase; PDBTitle: crystal structure of processing alpha-glucosidase i
73	d1lnsa2	Alignment	not modelled	23.0	18	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
74	c2k85A_	Alignment	not modelled	21.8	18	PDB header: protein binding Chain: A: PDB Molecule: glucocorticoid receptor dna-binding factor 1; PDBTitle: p190-a rhogap ff1 domain
75	c5x32B_	Alignment	not modelled	21.4	14	PDB header: isomerase Chain: B: PDB Molecule: n-acylglucosamine 2-epimerase; PDBTitle: crystal structure of d-mannose isomerase
76	c4bojC_	Alignment	not modelled	20.2	11	PDB header: hydrolase Chain: C: PDB Molecule: alpha-1,6-mannanase; PDBTitle: crystal structure of bacillus circulans tn-31 aman6 in2 complex with mannobiose
77	d2nvpal	Alignment	not modelled	19.6	15	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
78	c4z4lA_	Alignment	not modelled	19.2	14	PDB header: isomerase Chain: A: PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of cellobiose 2-epimerase from caldicellulosiruptor2 saccharolyticus dsm 8903
79	c3d82A_	Alignment	not modelled	19.1	21	PDB header: metal binding protein Chain: A: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
80	c5zhhB_	Alignment	not modelled	18.1	10	PDB header: isomerase Chain: B: PDB Molecule: cellobiose 2-epimerase; PDBTitle: structure of cellobiose 2-epimerase from bacillus

						thermoamylovorans2 b4167
81	c5c0rA_	Alignment	not modelled	17.9	12	PDB header: viral protein/immune system Chain: A: PDB Molecule: hemagglutinin, envelope glycoprotein, fibrinin fusion PDBTitle: crystal structure of a generation 3 influenza hemagglutinin stabilized2 stem complexed with the broadly neutralizing antibody c179
82	c4fusA_	Alignment	not modelled	17.5	18	PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related ca2+-binding protein; PDBTitle: the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
83	c2ky8A_	Alignment	not modelled	16.9	44	PDB header: transcription/dna Chain: A: PDB Molecule: methyl-cpg-binding domain protein 2; PDBTitle: solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
84	c5no8A_	Alignment	not modelled	16.7	21	PDB header: lyase Chain: A: PDB Molecule: baccell_00875; PDBTitle: polysaccharide lyase baccell_00875
85	c4c1sA_	Alignment	not modelled	15.8	14	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 76 mannosidase; PDBTitle: glycoside hydrolase family 76 (mannosidase) bt3792 from2 bacteroides thetaiotaomicron vpi-5482
86	c3fjsC_	Alignment	not modelled	15.5	16	PDB header: biosynthetic protein Chain: C: PDB Molecule: uncharacterized protein with rmlc-like cupin fold; PDBTitle: crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
87	c5mmi7_	Alignment	not modelled	15.1	33	PDB header: ribosome Chain: 7: PDB Molecule: 50s ribosomal protein 6, chloroplastic; PDBTitle: structure of the large subunit of the chloroplast ribosome
88	c5j4fB_	Alignment	not modelled	15.0	6	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminally his6-tagged hp0902, an2 uncharacterized protein from helicobacter pylori 26695
89	c5mlc8_	Alignment	not modelled	14.9	33	PDB header: ribosome Chain: 8: PDB Molecule: psrp6, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
90	d2e45a1	Alignment	not modelled	14.5	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
91	c2avpA_	Alignment	not modelled	14.0	17	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
92	d1g0wa1	Alignment	not modelled	13.7	16	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
93	d1sfua_	Alignment	not modelled	13.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
94	d1qh4a1	Alignment	not modelled	12.6	16	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
95	c6ar6A_	Alignment	not modelled	12.5	10	PDB header: toxin/protein binding Chain: A: PDB Molecule: toxin b; PDBTitle: clostridioides difficile toxinb with dld-4 darpin
96	c4e2gE_	Alignment	not modelled	12.4	16	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: cupin 2 conserved barrel domain protein; PDBTitle: crystal structure of cupin fold protein sthe2323 from sphaerobacter2 thermophilus
97	d2ysca1	Alignment	not modelled	12.4	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
98	c4kkkA_	Alignment	not modelled	12.4	17	PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
99	d1l6ja1	Alignment	not modelled	12.3	13	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain